STN

L3

32 L1 AND PY<=2002

FIL MEDLINE BIOSIS EMBASE SCISEARCH CAPLUS USPATFULL PCTFULL => s sodium and channel and polymorphism and (hh1b or hh1?)

L1 61 SODIUM AND CHANNEL AND POLYMORPHISM AND (HH1B OR HH1?)
=> dup rem 11
PROCESSING COMPLETED FOR L1

L2 53 DUP REM L1 (8 DUPLICATES REMOVED)
=> s 11 and py<=2002
2 FILES SEARCHED...
4 FILES SEARCHED...

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 5, 2004, 20:37:48 ; Search time 22471 Seconds Run on:

(without alignments)

11748.584 Million cell updates/sec

Title:

US-10-077-054-1

Perfect score: 6091

Sequence:

1 gatgagaagatggcaaactt.....ggccaggacacactgaaaag 6091

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched:

3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb ov:*
- 6: gb pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb sy:*
- 13: qb un:*
- 14: gb vi:*
- 15: em ba:*
- 16: em fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em sts:*

```
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_rod:*
36: em_htg_wam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*
```

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				
No.	Score	-	Length	DB	ID	Description
1	6091	100.0	6091	9	AF482988	AF482988 Homo sapi
2	6079.8	99.8	8414	9	AY038064	AY038064 Homo sapi
3	6075.6	99.7	6169	9	AY148488	AY148488 Homo sapi
4	6039.6	99.2	8491	6	AX449276	AX449276 Sequence
5	6039.6	99.2	8491	6	AX741279	AX741279 Sequence
6	6039.6	99.2	8491	_ 9	HUMHH1A	M77235 Human cardi
7	6038	99.1	8491	6	AX449278	AX449278 Sequence
8	5993.6	98.4	6048	6	AR183727	AR183727 Sequence
9	5990.4	98.3	6048	6	AR337848	AR337848 Sequence
10	5385.4	88.4	8530	6	AX552195	AX552195 Sequence
11	5119.6	84.1	6394	4	CFA555547	AJ555547 Canis fam
12	5094	83.6	6503	4	BTA251721	AJ251721 Bos tauru
13	5014.8	82.3	7545	10	RATSCAL	M27902 Rat cardiac
14	5013.4	82.3	6458	10	MMU271477	AJ271477 Mus muscu
15	4727.6	77.6	5901	6	AX348083	AX348083 Sequence
16	4727.6	77.6	5901	10	AF353637	AF353637 Rattus no
17	2553.6	41.9	6527	6	A58859	A58859 Sequence 7
18	2553.6	41.9	6527	6	AR230064	AR230064 Sequence
19	2550.8	41.9	6524	6	A58853	A58853 Sequence 1
20	2550.8	41.9	6524	6	AR230061	AR230061 Sequence
21	2550.8	41.9	6524	6	AX710158	AX710158 Sequence
22	2550.8	41.9	6524	10	RNSNS	X92184 R.norvegicu
23	2549.6	41.9	6344	6	AR253318	AR253318 Sequence
24	2549.6	41.9	6344	6	AX252389	AX252389 Sequence
25	2549.6	41.9	6344	10	RNU53833	U53833 Rattus norv
26	2508.8	41.2	6726	4	CFU60590	U60590 Canis famil
27	2487	40.8	5874	6	AR253325	AR253325 Sequence
28	2485.4	40.8	5874	6	AX252393	AX252393 Sequence
29	2485.4	40.8	5874	6	AX710162	AX710162 Sequence
30	2485.4	40.8	5874	9	AF117907	AF117907 Homo sapi
31	2432.8	39.9	6373	6	AX252391	AX252391 Sequence
32	2432.8	39.9	6373	10	MMSNS	Y09108 M.musculus
33	2243	36.8	6007	6	AR181336	AR181336 Sequence

34 35 36 37 38 39 40 41 42 43	2243 2225.4 2221.6 2221.6 2214.4 2214.4 2214.4 2204.2 2167.4	36.8 36.5 36.5 36.4 36.4 36.4 36.2 35.6	6586 6586 7052 7052 5977 6556 6556 5937 6826	10 6 6 6 6 10 10	AF049240 AR181360 A58857 AR230063 AR181335 AR181338 AF049239 AF049617 AR181339	AF049240 Rattus no AR181360 Sequence A58857 Sequence 5 AR230063 Sequence AR181335 Sequence AR181338 Sequence AF049239 Rattus no AF049617 Mus muscu AR181339 Sequence